



SEQUENCE LISTING

#5

<110> Kobilka, Brian H.
Ghanouni, Pejman
Lee, Tae Weon

<120> Conformational assays to detect binding
to G protein-coupled receptors

<130> STAN213

<140> 09/935,061

<141> 2001-08-21

<150> 60/286,250

<151> 2001-04-24

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 2

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 2

Asp Tyr Lys Asp Glu Asp Asp Lys

1

5

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 3

Ala Trp Arg His Pro Gln Phe Gly Gly

1

5

<210> 4

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 4

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg

1

5

10

<210> 5

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<400> 5

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga

48

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg

1

5

10

15

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg

96

Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp

20

25

30

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg

144

Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val

35

40

45

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg

192

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu

50

55

60

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg

240

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu

65

70

75

80

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg

288

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met

85	90	95	
aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att			336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile			
100	105	110	
gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca			384
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala			
115	120	125	
gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg			432
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu			
130	135	140	
ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg			480
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val			
145	150	155	160
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc			528
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala			
165	170	175	
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac			576
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp			
180	185	190	
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc			624
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe			
195	200	205	
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag			672
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln			
210	215	220	
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc			720
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe			
225	230	235	240
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat			768
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His			
245	250	255	
gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag cac aaa gcc ctc			816
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu			
260	265	270	
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc			864
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro			
275	280	285	
ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt			912

Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg
 290 295 300
 aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt 960
 Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly
 305 310 315 320
 ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc 1008
 Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe
 325 330 335
 cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat 1056
 Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn
 340 345 350
 ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg 1104
 Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val
 355 360 365
 gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg 1152
 Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
 370 375 380
 gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat 1200
 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
 385 390 395 400
 tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg 1239
 Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 405 410

<210> 6
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
 1 5 10 15
 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
 20 25 30
 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
 35 40 45
 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
 50 55 60
 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
 65 70 75 80
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
 85 90 95
 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile

	100		105		110										
Asp	Val	Leu	Cys	Val	Thr	Ala	Ser	Ile	Glu	Thr	Leu	Cys	Val	Ile	Ala
	115		120		125										
Val	Asp	Arg	Tyr	Phe	Ala	Ile	Thr	Ser	Pro	Phe	Lys	Tyr	Gln	Ser	Leu
	130		135		140										
Leu	Thr	Lys	Asn	Lys	Ala	Arg	Val	Ile	Ile	Leu	Met	Val	Trp	Ile	Val
	145		150		155										
Ser	Gly	Leu	Thr	Ser	Phe	Leu	Pro	Ile	Gln	Met	His	Trp	Tyr	Arg	Ala
			165		170										
Thr	His	Gln	Glu	Ala	Ile	Asn	Cys	Tyr	Ala	Asn	Glu	Thr	Cys	Cys	Asp
			180		185										
Phe	Phe	Thr	Asn	Gln	Ala	Tyr	Ala	Ile	Ala	Ser	Ser	Ile	Val	Ser	Phe
	195		200		205										
Tyr	Val	Pro	Leu	Val	Ile	Met	Val	Phe	Val	Tyr	Ser	Arg	Val	Phe	Gln
	210		215		220										
Glu	Ala	Lys	Arg	Gln	Leu	Gln	Lys	Ile	Asp	Lys	Ser	Glu	Gly	Arg	Phe
	225		230		235										
His	Val	Gln	Asn	Leu	Ser	Gln	Val	Glu	Gln	Asp	Gly	Arg	Thr	Gly	His
			245		250										
Gly	Leu	Arg	Arg	Ser	Ser	Lys	Phe	Cys	Leu	Lys	Glu	His	Lys	Ala	Leu
	260		265		270										
Lys	Thr	Leu	Gly	Ile	Ile	Met	Gly	Thr	Phe	Thr	Leu	Cys	Trp	Leu	Pro
	275		280		285										
Phe	Phe	Ile	Val	Asn	Ile	Val	His	Val	Ile	Gln	Asp	Asn	Leu	Ile	Arg
	290		295		300										
Lys	Glu	Val	Tyr	Ile	Leu	Leu	Asn	Trp	Ile	Gly	Tyr	Val	Asn	Ser	Gly
	305		310		315										
Phe	Asn	Pro	Leu	Ile	Tyr	Cys	Arg	Ser	Pro	Asp	Phe	Arg	Ile	Ala	Phe
			325		330										
Gln	Glu	Leu	Leu	Cys	Leu	Arg	Arg	Ser	Ser	Leu	Lys	Ala	Tyr	Gly	Asn
	340		345		350										
Gly	Tyr	Ser	Ser	Asn	Gly	Asn	Thr	Gly	Glu	Gln	Ser	Gly	Tyr	His	Val
	355		360		365										
Glu	Gln	Glu	Lys	Glu	Asn	Lys	Leu	Leu	Cys	Glu	Asp	Leu	Pro	Gly	Thr
	370		375		380										
Glu	Asp	Phe	Val	Gly	His	Gln	Gly	Thr	Val	Pro	Ser	Asp	Asn	Ile	Asp
	385		390		395										
Ser	Gln	Gly	Arg	Asn	Cys	Ser	Thr	Asn	Asp	Ser	Leu	Leu			
			405		410										

<210> 7

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 2nd
intracellular loop

<221> CDS

<222> (1)...(1239)

<400> 7

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga	48
Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	
agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	
gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	
ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	
cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	
gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	
aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	
gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca	384
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala	
115 120 125	
gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg	432
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	
130 135 140	
ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg	480
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	
145 150 155 160	
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc	528
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	
165 170 175	
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac	576
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	
180 185 190	
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc	624
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	

195	200	205	
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln 210 215 220			672
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe 225 230 235 240			720
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His 245 250 255			768
gga ctc gaa aac ctc tac ttc cag ggg ttg aag gag cac aaa gcc ctc Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu 260 265 270			816
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro 275 280 285			864
ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg 290 295 300			912
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly 305 310 315 320			960
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe 325 330 335			1008
cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn 340 345 350			1056
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val 355 360 365			1104
gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr 370 375 380			1152
gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp 385 390 395 400			1200
tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg			1239

Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 405 410

<210> 8
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Beta-2 Adrenergic Receptor with TEV site in 2nd
 intracellular loop

<400> 8
 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
 1 5 10 15
 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
 20 25 30
 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
 35 40 45
 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
 50 55 60
 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
 65 70 75 80
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
 85 90 95
 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
 100 105 110
 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
 115 120 125
 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
 130 135 140
 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
 165 170 175
 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
 195 200 205
 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
 210 215 220
 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
 225 230 235 240
 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
 245 250 255
 Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu
 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
 275 280 285
 Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg

290		295		300
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly				
305		310		320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe				
	325		330	335
Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn				
	340		345	350
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val				
	355		360	365
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr				
	370		375	380
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp				
385		390		400
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu				
	405		410	

<210> 9

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 3rd intracellular loop

<221> CDS

<222> (1)...(1251)

<400> 9

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga	48
Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	
agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	
gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	
ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	
cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	
gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	

85	90	95	
aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att			336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile			
100	105	110	
gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca			384
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala			
115	120	125	
gtg gat cgc tac ttt gcc att act tca cct ttc aag gag aat ctc tac			432
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu Tyr			
130	135	140	
ttc cag ggc ctg ctg acc aag aat aag gcc cgg gtg atc att ctg atg			480
Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met			
145	150	155	160
gtg tgg att gtg tca ggc ctt acc tcc ttc ttg ccc att cag atg cac			528
Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His			
165	170	175	
tgg tac cgg gcc acc cac cag gaa gcc atc aac tgc tat gcc aat gag			576
Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu			
180	185	190	
acc tgc tgt gac ttc ttc acg aac caa gcc tat gcc att gcc tct tcc			624
Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser			
195	200	205	
atc gtg tcc ttc tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc			672
Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser			
210	215	220	
agg gtc ttt cag gag gcc aaa agg cag ctc cag aag att gac aaa tct			720
Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser			
225	230	235	240
gag ggc cgc ttc cat gtc cag aac ctt agc cag gtg gag cag gat ggg			768
Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly			
245	250	255	
cgg acg ggg cat gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag			816
Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu			
260	265	270	
cac aaa gcc ctc aag acg tta ggc atc atc atg ggc act ttc acc ctc			864
His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu			
275	280	285	
tgc tgg ctg ccc ttc ttc atc gtt aac att gtg cat gtg atc cag gat			912

Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp	
290 295 300	
aac ctc atc cgt aag gaa gtt tac atc ctc cta aat tgg ata ggc tat	960
Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr	
305 310 315 320	
gtc aat tct ggt ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc	1008
Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe	
325 330 335	
agg att gcc ttc cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag	1056
Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys	
340 345 350	
gcc tat ggg aat ggc tac tcc agc aac ggc aac aca ggg gag cag agt	1104
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser	
355 360 365	
gga tat cac gtg gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac	1152
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp	
370 375 380	
ctc cca ggc acg gaa gac ttt gtg ggc cat caa ggt act gtg cct agc	1200
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser	
385 390 395 400	
gat aac att gat tca caa ggg agg aat tgt agt aca aat gac tca ctg	1248
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu	
405 410 415	
ctg	1251
Leu	

<210> 10
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Beta-2 Adrenergic Receptor with TEV site in 3rd
 intracellular loop

<400> 10
 Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
 1 5 10 15
 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
 20 25 30
 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val

<211> 1176
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (1)...(1176)

<400> 11
 atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc 48
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15

ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc 96
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac 144
 Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt 192
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg 240
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc 288
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt 336
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg 384
 Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
 115 120 125

aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata 432
 Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
 130 135 140

gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc 480
 Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
 145 150 155 160

tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag 528
 Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys

165	170	175	
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc			576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct			624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct			672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc			720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg			768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa			816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg			864
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val			
275	280	285	
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att			912
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile			
290	295	300	
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg			960
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp			
305	310	315	320
cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc			1008
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val			
325	330	335	
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc			1056
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe			
340	345	350	
tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att			1104
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile			
355	360	365	
cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga			1152

Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
 370 375 380

act aat cat cag gta cgc agt ctc
 Thr Asn His Gln Val Arg Ser Leu
 385 390

1176

<210> 12
 <211> 392
 <212> PRT
 <213> homo sapiens

<400> 12
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30
 Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110
 Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
 115 120 125
 Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
 130 135 140
 Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
 145 150 155 160
 Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
 165 170 175
 Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
 180 185 190
 Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala
 195 200 205
 Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
 210 215 220
 His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile
 225 230 235 240
 Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
 245 250 255
 Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
 260 265 270
 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile

290	295	300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp		
305	310	315
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val		
	325	330
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe		
	340	345
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile		
	355	360
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg		
	370	375
Thr Asn His Gln Val Arg Ser Leu		380
385	390	

<210> 13
 <211> 1176
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> μ Opioid receptor with TEV site in 2nd
 intracellular loop

<221> CDS
 <222> (1)...(1176)

<400> 13	
atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc	48
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	
1 5 10 15	
ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc	96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	
20 25 30	
aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac	144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	
35 40 45	
cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt	192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	
50 55 60	
ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg	240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	
65 70 75 80	
tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc	288
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	
85 90 95	

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt	336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	
100 105 110	
gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg	384
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	
115 120 125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata	432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile	
130 135 140	
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc	480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu	
145 150 155 160	
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag	528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys	
165 170 175	
gaa aac ctc tac ttc cag ggg cga aat gcc aaa att atc aat gtc tgc	576
Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys	
180 185 190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct	624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala	
195 200 205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct	672
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser	
210 215 220	
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc	720
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile	
225 230 235 240	
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg	768
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu	
245 250 255	
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa	816
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu	
260 265 270	
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg	864
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val	
275 280 285	
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att	912
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile	
290 295 300	

aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg 960
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320

 cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc 1008
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335

 ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc 1056
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350

 tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att 1104
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
 355 360 365

 cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga 1152
 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
 370 375 380

 act aat cat cag gta cgc agt ctc 1176
 Thr Asn His Gln Val Arg Ser Leu
 385 390

<210> 14
 <211> 392
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> μ Opioid receptor with TEV site in 2nd
 intracellular loop

<400> 14
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30
 Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110
 Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val

115	120	125
Asn Tyr Leu Met Gly Thr Trp	Pro Phe Gly Thr Ile	Leu Cys Lys Ile
130	135	140
Val Ile Ser Ile Asp Tyr Tyr	Asn Met Phe Thr Ser	Ile Phe Thr Leu
145	150	155
Cys Thr Met Ser Val Asp Arg Tyr	Ile Ala Val Cys His	Pro Val Lys
165	170	175
Glu Asn Leu Tyr Phe Gln Gly Arg	Asn Ala Lys Ile Ile	Asn Val Cys
180	185	190
Asn Trp Ile Leu Ser Ser Ala Ile	Gly Leu Pro Val Met	Phe Ile Ala
195	200	205
Thr Thr Lys Tyr Arg Gln Gly Ser	Ile Asp Cys Thr Leu	Thr Phe Ser
210	215	220
His Pro Thr Trp Tyr Trp Glu	Asn Leu Leu Lys Ile	Cys Val Phe Ile
225	230	235
Phe Ala Phe Ile Met Pro Val Leu	Ile Ile Thr Val Cys	Tyr Gly Leu
245	250	255
Met Ile Leu Arg Leu Lys Ser Val	Arg Met Leu Ser Gly	Ser Lys Glu
260	265	270
Lys Asp Arg Asn Leu Arg Arg Ile	Thr Arg Met Val Leu	Val Val Val
275	280	285
Ala Val Phe Ile Val Cys Trp Thr	Pro Ile His Ile Tyr	Val Ile Ile
290	295	300
Lys Ala Leu Val Thr Ile Pro Glu	Thr Thr Phe Gln Thr	Val Ser Trp
305	310	315
His Phe Cys Ile Ala Leu Gly Tyr	Thr Asn Ser Cys Leu	Asn Pro Val
325	330	335
Leu Tyr Ala Phe Leu Asp Glu Asn	Phe Lys Arg Cys Phe	Arg Glu Phe
340	345	350
Cys Ile Pro Thr Ser Ser Asn Ile	Glu Gln Gln Asn Ser	Thr Arg Ile
355	360	365
Arg Gln Asn Thr Arg Asp His Pro	Ser Thr Ala Asn Thr	Val Asp Arg
370	375	380
Thr Asn His Gln Val Arg Ser Leu		
385	390	

<210> 15
 <211> 1197
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> μ Opioid receptor with TEV site in 3rd
 intracellular loop

<221> CDS
 <222> (1)...(1197)

<400> 15
 atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala

48

1	5	10	15	
ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc				96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val				
	20	25	30	
aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac				144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn				
	35	40	45	
cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt				192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser				
	50	55	60	
ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg				240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val				
	65	70	75	80
tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc				288
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val				
	85	90	95	
aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt				336
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu				
	100	105	110	
gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg				384
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val				
	115	120	125	
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata				432
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile				
	130	135	140	
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc				480
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu				
	145	150	155	160
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag				528
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys				
	165	170	175	
gcc tta gat ttc cgt act ccc cga aat gcc aaa att atc aat gtc tgc				576
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys				
	180	185	190	
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct				624
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala				
	195	200	205	
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct				672

Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser		
210						215					220						
cat	cca	acc	tgg	tac	tgg	gaa	aac	ctg	ctg	aag	atc	tgt	gtt	ttc	atc	720	
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile		
225					230					235					240		
ttc	gcc	ttc	att	atg	cca	gtg	ctc	atc	att	acc	gtg	tgc	tat	gga	ctg	768	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu		
				245					250					255			
atg	atc	ttg	cgc	ctc	aag	agt	gtc	cgc	atg	ctc	tct	ggc	tcc	aaa	gaa	816	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu		
			260					265					270				
aag	gac	gaa	aac	ctc	tac	ttc	cag	ggg	agg	aat	ctt	cga	agg	atc	acc	864	
Lys	Asp	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Arg	Asn	Leu	Arg	Arg	Ile	Thr		
		275					280					285					
agg	atg	gtg	ctg	gtg	gtg	gtg	gct	gtg	ttc	atc	gtc	tgc	tgg	act	ccc	912	
Arg	Met	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro		
	290					295					300						
att	cac	att	tac	gtc	atc	att	aaa	gcc	ttg	gtt	aca	atc	cca	gaa	act	960	
Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr		
305					310					315					320		
acg	ttc	cag	act	gtt	tct	tgg	cac	ttc	tgc	att	gct	cta	ggg	tac	aca	1008	
Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr		
				325					330					335			
aac	agc	tgc	ctc	aac	cca	gtc	ctt	tat	gca	ttt	ctg	gat	gaa	aac	ttc	1056	
Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe		
			340					345					350				
aaa	cga	tgc	ttc	aga	gag	ttc	tgt	atc	cca	acc	tct	tcc	aac	att	gag	1104	
Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu		
		355					360						365				
caa	caa	aac	tcc	act	cga	att	cgt	cag	aac	act	aga	gac	cac	ccc	tcc	1152	
Gln	Gln	Asn	Ser	Thr	Arg	Ile	Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser		
		370					375				380						
acg	gcc	aat	aca	gtg	gat	aga	act	aat	cat	cag	gta	cgc	agt	ctc		1197	
Thr	Ala	Asn	Thr	Val	Asp	Arg	Thr	Asn	His	Gln	Val	Arg	Ser	Leu			
385					390					395							

<210> 16
 <211> 399
 <212> PRT

<213> Artificial Sequence

<220>

<223> μ Opioid receptor with TEV site in 3rd
intracellular loop

<400> 16

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5				10						15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asp	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asp	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
65					70					75				80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
				85					90					95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
		115					120					125			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130					135					140				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
145					150					155				160	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
				165					170					175	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
			180					185					190		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Ile	Ala
		195					200					205			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210					215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile
225					230					235				240	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
			245						250					255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
		260						265					270		
Lys	Asp	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Arg	Asn	Leu	Arg	Arg	Ile	Thr
		275					280					285			
Arg	Met	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro
	290					295					300				
Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr
305				310						315				320	
Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr
			325						330					335	
Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe
			340					345					350		

Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu
		355					360					365			
Gln	Gln	Asn	Ser	Thr	Arg	Ile	Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser
	370					375					380				
Thr	Ala	Asn	Thr	Val	Asp	Arg	Thr	Asn	His	Gln	Val	Arg	Ser	Leu	
385					390					395					